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**PATENT APPLICATION**

**TAG NUCLEIC ACIDS AND PROBE ARRAYS**

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# **TAG NUCLEIC ACIDS AND PROBE ARRAYS**

## **PRIORITY CLAIM**

This application claims priority of U.S. Provisional Application 60/195,585 filed April 6, 2000 entitled "Tag Nucleic Acids and Probe Arrays", which is incorporated herein by reference for all purposes in its entirety.

## **FIELD OF THE INVENTION**

This invention provides sets of nucleic acid tags, arrays of oligonucleotide probes, nucleic acid-tagged sets of recombinant cells and other compositions. The invention relates to the selection and interaction of nucleic acids, and nucleic acids immobilized to solid substrates, including related chemistry, biology, and medical diagnostic uses.

## **BACKGROUND OF THE INVENTION**

The use of short nucleic acid sequences as "tags" to identify specific biological substances in a sample is known. For example, tags may be used as a method of or as labels for a wide variety of biological and nonbiological materials, see, for example, Dollinger, The Polymerase Chain Reaction pp. 265-274 Mullis et al., editors (Birkhauser, Boston, 1994) or as a method of screening complex chemical libraries. See, for example, Alper, Science, 264: 1399-1401 (1994); and Needels et al. PNAS 90, 10700-10704 (1993). See also US Patent Nos. 4,359,353, 4,441,943, 5,451,505 and 5,654,413.

There is great necessity for sets of tag sequences which are known to hybridize effectively to their complementary probe sequences with minimal cross-hybridization between the different tag sequences. The presently claimed invention provides sets of tag sequences, tag sequence kits, and methods of using tag sequences which fulfill these requirements.

## **SUMMARY OF THE INVENTION**

The presently claimed invention provides 2050 unique sequences which have been specifically chosen according to strict criteria to produce sequences suitable for a wide variety of “tagging” applications. These sequences are provided as SEQ ID NOs 1-2050.

In one embodiment, some or all of SEQ ID Nos 1-2050 comprise tag sequences. In a further embodiment, some or all of SEQ ID Nos 1-2050 comprise tag-probe sequences. In a further embodiment, the tag-probe sequences are immobilized to a solid support.

The unique sequences of the presently claimed invention may be used alone or in combinations of 10 or more, 100 or more, 200 or more, 500 or more, 1000 or more, 1500 or more, or 2000 or more as nucleic acid tags and/or tag-probes.

## **BRIEF DESCRIPTION OF THE DRAWINGS**

FIG. 1 shows a plot of the discrimination score and the signal intensity for 2200 candidate sequences.

FIG. 2 shows an example of the sequences attached to each of the four array features representing a given tag sequence. Four features, organized vertically on the probe array, represent each tag-probe.

FIG. 3 shows the array features from an array designed to probe for the tag sequences of the presently claimed invention. For each of the four tag-probes shown, arranged horizontally across the array, the brightest hybridization signal is seen with the “PM” feature.

FIG. 4 is a scanned image of the hybridization patterns resulting from the hybridization of 2050 different probes containing regions complementary to the SEQ ID Nos 1-2050 to an array comprised of tag-probes corresponding to SEQ ID Nos 1-2050.

FIG. 5 is a scanned image of the hybridization patterns resulting from the hybridization of 50 different probes containing regions complementary to SEQ ID Nos 2001-2050 to an array identical to the array depicted in FIG. 4.

FIG. 6 shows signal intensities from two different independent experiments in which 2000 biotinylated oligonucleotide tags or 50 fluorescein labeled control oligonucleotides were hybridized to arrays designed as described above.

FIG. 7 shows the PM/MM ratios from the data described in FIG. 4 above.

## **DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS**

### **I. Definitions**

As used herein, certain terms may have the following defined meanings.

As used in the specification and claims, the singular forms “a”, “an” and “the” include plural references unless the context clearly dictates otherwise. For example, the term “an array” may include a plurality of arrays unless the context clearly dictates otherwise.

An “array” represents an intentionally created collection of molecules which can be prepared either synthetically or biosynthetically. In particular, the term “array” herein means an intentionally created collection of polynucleotides attached to at least a first surface of at least one solid support wherein the identity of each polynucleotide at a given predefined region is known. The terms “array,” “biological chip” and “chip” are used interchangeably.

The array of molecules can be screened for biological activity in a variety of different formats (e.g., libraries of soluble molecules, libraries of compounds tethered to resin beads, fibers, silica chips, or other solid supports). The fabrication of polynucleotide arrays on a solid substrate, and methods of use of the arrays in different assays, are described in US Patent Numbers: 5,143,854, 5,242,979, 5,252,743, 5,324,663, 5,384,261, 5,405,783, 5,412,087, 5,424,186, 5,445,934, 5,451,683, 5,482,867, 5,489,678, 5,491,074, 5,510,270, 5,527,681, 5,550,215, 5,571,639, 5,593,839, 5,599,695, 5,624,711, 5,631,734, 5,677,195, 5,744,101, 5,744,305, 5,744,992, 5,753,788, 5,770,456, 5,831,070, 5,856,011, 6,040,138 and 6,040,193 all of which are incorporated by reference herein in their entireties for all purposes. See also, US Serial Nos. 09/079,324, 09/122,216, and PCT Application WO US99/00730 each of which is incorporated by reference herein in its entirety for all purposes. Preferred arrays contemplated by the presently claimed invention have the probe densities as described in the above referenced patents. For example, the ‘305 patent discloses 100, 400, 1,000 and 10,000 probes/cm<sup>2</sup>.

"Solid support," "support," and "substrate" refer to a material or group of materials having a rigid or semi-rigid surface or surfaces. In many embodiments, at least one surface of the solid support will be substantially flat, although in some embodiments it may be desirable to physically separate synthesis regions for different compounds with, for example, wells, raised regions, pins, etched trenches, or the like. According to other embodiments, the solid support(s) will take the form of beads, resins, gels, microspheres, fibers or other geometric configurations.

A "discrete, known location" refers to a localized area on a solid support which is, was, or is intended to be used for placement or fabrication of a selected molecule and is otherwise referred to herein in the alternative as a "selected" region. The discrete, known location may have any convenient shape, *e.g.*, circular, rectangular, elliptical, wedge-shaped, etc. For the sake of brevity herein, "discrete, known locations" are sometimes referred to as "predefined regions," "regions," or "features." In some embodiments, a discrete, known location and, therefore, the area upon which each distinct compound is synthesized is smaller than about 1 cm<sup>2</sup> or even less than 1 mm<sup>2</sup>. In additional embodiments, a discrete, known location can be achieved by physically separating the regions (*i.e.*, beads, fibers, resins, gels, etc.) into wells, trays, etc.

As used herein, a "polynucleotide" is a sequence of two or more nucleotides. Polynucleotides of the present invention include sequences of deoxyribonucleic acid (DNA) or ribonucleic acid (RNA) which may be isolated from natural sources, recombinantly produced, or artificially synthesized. A further example of a polynucleotide of the present invention may be polyamide polynucleotide or peptide nucleic acid (PNA). This invention also encompasses situations in which there is nontraditional base pairing such as Hoogsteen base pairing which has been identified in certain tRNA molecules and postulated to exist in a triple helix. "Polynucleotide" is used interchangeably with "oligonucleotide" in this application.

The terms "nucleotide" and "nucleic acid base" include deoxynucleotides and analogs thereof. These analogs are those molecules having some structural features in common with a naturally occurring nucleotide such that when incorporated into a polynucleotide sequence, they allow hybridization with a complementary polynucleotide in solution. Typically, these analogs may have one or more modified bases, as well as modified forms of ribose and phosphodiester moieties. The changes can be tailor made to stabilize or destabilize hybrid formation, enhance

the specificity of hybridization with a complementary polynucleotide sequence as desired, or enhance stability of the polynucleotide.

The terms "nucleic acid," "nucleic acid molecule," or "nucleic acid sequence," refer to a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, and unless otherwise limited, would encompass analogs of natural nucleotides that can function in a similar manner as naturally occurring nucleotides. Nucleic acids may be derived from a variety of sources including, but not limited to, naturally occurring nucleic acids, clones, synthesis in solution or solid phase synthesis.

As used herein a "probe" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.* A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "target nucleic acid" or "target sequence" refers to a nucleic acid or nucleic acid sequence which is to be analyzed. A target can be a nucleic acid to which a probe will hybridize. The probe may or may not be specifically designed to hybridize to the target. It is either the presence or absence of the target nucleic acid that is to be detected, or the amount of the target nucleic acid that is to be quantified. The term target nucleic acid may refer to the specific subsequence of a larger nucleic acid to which the probe is directed or to the overall sequence (*e.g.*, gene or mRNA) whose expression level it is desired to detect. The difference in usage will be apparent from context.

The term "hybridization" refers to the process in which two single-stranded polynucleotides bind non-covalently to form a stable double-stranded polynucleotide; triple-stranded hybridization is also theoretically possible. The resulting (usually) double-stranded polynucleotide is a "hybrid." The proportion of the population of polynucleotides that forms stable hybrids is referred to herein as the "degree of hybridization." Hybrids can contain two DNA strands, two RNA strands, or one DNA and one RNA strand.

Methods for conducting polynucleotide hybridization assays have been well developed in the art. Hybridization assay procedures and conditions will vary depending on the application and are selected in accordance with the general binding methods known including those referred to in: Molecular Cloning, A Laboratory Manual, Second Ed., J. Sambrook et al., Eds., Cold Spring Harbor Laboratory Press, 1989 ("Sambrook et al."); Berger and Kimmel, "Methods in Enzymology," Vol. 152, "Guide to Molecular Cloning Techniques", Academic Press, Inc., San Diego, CA., 1987; Young and Davis, *Proc. Natl. Acad. Sci., U.S.A.*, 80:1194 (1983), each of which are incorporated herein by reference.

It is appreciated that the ability of two single stranded polynucleotides to hybridize will depend upon factors such as their degree of complementarity as well as the stringency of the hybridization reaction conditions.

As used herein, "stringency" refers to the conditions of a hybridization reaction that influence the degree to which polynucleotides hybridize. Stringent conditions can be selected that allow polynucleotide duplexes to be distinguished based on their degree of mismatch. High stringency is correlated with a lower probability for the formation of a duplex containing mismatched bases. Thus, the higher the stringency, the greater the probability that two single-stranded polynucleotides, capable of forming a mismatched duplex, will remain single-stranded. Conversely, at lower stringency, the probability of formation of a mismatched duplex is increased.

A nucleic acid "tag" is a selected nucleic acid with a specified nucleic acid sequence. A nucleic acid "probe" hybridizes to a nucleic acid "tag."

A nucleic acid "tag-probe" is a specific sequence capable of hybridizing to a specific "tag." Typically, the "tag-probe" is the complement or a partial complement of the "tag." In one typical configuration, nucleic acid tags are incorporated as labels into biological libraries, and the tag nucleic acids are detected using a microarray.

Throughout this disclosure, various aspects of this invention are presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention.

Accordingly, the description of a range should be considered to have specifically disclosed all the possible sub-ranges as well as individual numerical values within that range. For example, the description of a range such as 4 to 50 should be considered to have specifically disclosed all integers within the sub-ranges such as 4 to 10, 4 to 20, 4 to 30, 4 to 40, 4 to 50, 5 to 10, 5 to 20 etc., as well as individual numbers within that range, for example, 6, 8, 15, 20, 32, 39, 43, 48 etc. This applies regardless of the breadth of the range. Likewise, a description of a range such as 1 or more, 10 or more,  $10^3$  or more,  $10^6$  or more, or  $10^{12}$  or more should be considered to have specifically disclosed individual numbers within that range as well as higher numbers, for example, 20,  $2 \times 10^4$ ,  $3 \times 10^8$ ,  $4 \times 10^{15}$ ,  $5 \times 10^{18}$ , etc.

Various patents, patent applications and publications are referenced throughout the specification, unless otherwise indicated, each is incorporated by reference in its entirety for all purposes.

## **II. General**

The presently claimed invention provides 2050 unique sequences which have been specifically chosen according to strict criteria to produce sequences suitable for a wide variety of “tagging” applications. These sequences are provided as SEQ ID NOs 1-2050.

In one embodiment, some or all of SEQ ID Nos 1-2050 comprise tag sequences. In a further embodiment, some or all of SEQ ID Nos 1-2050 comprise tag-probe sequences. In a further embodiment, the tag-probe sequences are immobilized to a solid support.

An initial set of 2200 20mer sequences was selected with closely matched melting temperatures. A further filter based on rules such as those described in US Provisional Patent Application 60/176,520 was applied to optimize and standardize the hybridization characteristics of the set. Finally, sequences were removed if they were identical or nearly identical to each other or to sequences in the public databases. This reduced the pool of candidate sequences to 2200. The hybridization performance of the entire set of 2200 candidate sequences was evaluated. Labeled oligonucleotides complementary to the candidate sequences were synthesized and hybridized to an array containing probes designed to analyze the performance of all 2200 candidate sequences. The array contained four different sequences to



interrogate each candidate sequence. A probe designed to be the perfect match complement to the candidate sequence (PM), a probe designed to have a central mismatch at position 10 (MM), and probes designed to be the complements to the PM and MM probes (cPM and cMM respectively).

FIG. 1 shows a plot of the discrimination score and the signal intensity for all 2200 sequences. A line was fitted to select the 2050 sequences with the highest discrimination and signal intensity. These 2050 sequences are SEQ ID Nos. 1-2050.

In one embodiment of the invention, the sequences of the presently claimed invention are tag-probes attached to a solid support. Methods of immobilizing presynthesized sequences and synthesizing sequences de novo on solid supports are known. See for example, US Patent Numbers: 5,143,854, 5,242,979, 5,252,743, 5,324,663, 5,384,261, 5,405,783, 5,412,087, 5,424,186, 5,445,934, 5,451,683, 5,482,867, 5,489,678, 5,491,074, 5,510,270, 5,527,681, 5,550,215, 5,571,639, 5,593,839, 5,599,695, 5,624,711, 5,631,734, 5,677,195, 5,744,101, 5,744,305, 5,753,788, 5,770,456, 5,831,070, 5,856,011, 5,744,992, 6,040,138, 6,040,193, US Serial Nos. 09/079,324, 09/122,216, and PCT Application WO US99/00730.

In this and other embodiments it is often useful to provide control probes. As one example, SEQ ID Nos. 1-2000 may comprise the tag-probes and SEQ ID Nos. 2001-2050 may comprise the control probes. In a preferred embodiment, the control probes are representative of the population with respect to observed signal intensities and discrimination. In a further preferred embodiment, tag sequences with relatively low signals may be over-represented in the control sequences so as to increase information about the sensitivity of experiments at the lower limit of detection.

## **METHODS OF USE**

The use of short nucleic acid sequences as “tags” to identify specific biological substances in a sample is known. For example, tags may be used as a method of or as labels for a wide variety of biological and nonbiological materials, see, for example, Dollinger, The Polymerase Chain Reaction pp. 265-274 Mullis et al., editors (Birkhauser, Boston, 1994) or as a method of screening complex chemical libraries. See, for example, Brenner and Lerner, PNAS

89, 5281-5383 (1992); Alper, Science, 264: 1399-1401 (1994); and Needels et al. PNAS 90, 10700-10704 (1993). See also US Patent Nos. 4,359,353, 4,441,943, 5,451,505 5,149,625, 5,654,413 and 5,800,992.

In addition to those applications above, the presently claimed sequences are suitable to be employed for any of the methods described in US Patent Application No. 08/626,285 (filed 4/4/96), including as a method of analysis of genomic DNA. For example, as described in the '285 application, tag arrays may be used to identify the function of identified open reading frames (ORFs) by creating deletion mutants for each ORF and analyzing the resulting deletion mutants under a wide variety of selective conditions.

US Provisional Patent Application No. 60/140,359 (filed 6/23/99) described methods of using tag arrays and the single base extension reaction for genotyping and other types of biological analysis. A set of tags and a tag array derived from Seq. ID Nos. 1-2000 and their complements are suitable to be used for the methods described in this application. Briefly, the '359 application describes methods of determining the genotype of an individual at a polymorphic locus or the frequency of alleles in a population. One embodiment of the method involves three step: (1) amplification of the polymorphic locus, (2) primer extension of a sequence-tagged primer with distinct labels for different polynucleotides at the polymorphic locus, and (3) hybridization to a tag array. The amount of each distinct label can be determined at known positions of the tag array. Each tag represents a distinct polymorphic locus and each distinct label represents a distinct allelic form at the polymorphic locus. The method permits the simultaneous determination of a genotype at multiple loci, as well as the determination of allele frequencies in a population. Another embodiment employs just steps (2) and (3).

Table 1, below, lists the sequences of the presently claimed invention. Column 1 lists the sequence ID number corresponding to each sequence. Column 2 lists the sequences in the 3' to 5' direction.

**TABLE I**

Seq. Id	3' to 5' sequence
1	TAAACTAGCATTGAGCCCAC
2	AAATCAGCAAACGGGCTCCG
3	GAATTGATAATCGCAGCCAC
4	GATATAGGAATGGCGCATAC



Seq. Id	3' to 5' sequence
53	CATTGCGAACTGCATCTAAC
54	GATAGTCCAATGCTACTGAC
55	GATT CGGTAATGCGCTGTAA
56	GACGTTTCAATGCAGCGTAA
57	GAGAGTGCAATGCCGACTAA
58	GAGATCCGAATGCGCGTACT
59	CGAGATCCAAGGCCCATGAT
60	AGCTTGACACAGTAACCATGA
61	AGAGTTGAACAGCATACCT
62	TATCTGATCGGACGGCCAGT
63	TATTGACTACTGCGCCTCAG
64	TTGGACTATTGGGTATCGCC
65	TTGTCAGATTGGATGCGCTC
66	TATGCAGAATGGCGTGTATC
67	CATTGGATAAGCACTGATCG
68	CCCGGAATAAGGCCACGATA
69	CTCATAGAATGGACCAGATC
70	CATAGATTAAGCACTCAGCC
71	CATGATGTAAGCACGCTACC
72	CAGGAGCGAAGCAGATACTC
73	CAGAGCAGAAGCACTCACGT
74	TACATAGGCTTCAGCATCAC
75	TATTATACCTTGATCCGCGC
76	TAAACTGCTTGCATACGGCG
77	TATAAGCCTTGCAGCGGACC
78	TTTAAGCGGTGGATCTAGCT
79	TTAATAGCCTTGAGCAGCGA
80	ATAAATGCTTGAACCCCTCG
81	GAAAGTTCATGGAATCGAGC
82	GCAAGGATTCGACTCAGAC
83	CAAAGAATAATCGCTCCTCG
84	TAAAGCACTTATGACTCGGC
85	TTATAGCATTCTGTAGGCGC
86	TCGCTGACATTTGATTAGCC
87	CCTTGAATAATATCTCGGCC
88	AGGTCCAGAAATTGCTGCAC
89	AGCTCAGGAAATTCTAGCGA
90	AGCTATGCAAATTAGAGGCC
91	GGTAGGCTAATTTATGGCAC
92	CTAATGCAATTCATGCCGC
93	CAACTGGCAATCAATACGCT
94	CCAAGCGAATGCAACGTATC
95	GCATAGCGAATTGGAGATAC
96	GCATGTGCAATGGATGATAC
97	GCACGTTCAATGGCTCGACT
98	GCAGCGCAATCTGTCGAGTA
99	AGCAGTGCAAATCCTGATAC
100	AGCTTCGCAAATCTGGTACA

Attorney Docket No. 3108.1

Seq. Id	3' to 5' sequence
101	AGCCTGCGAAATCTACTGAA
102	GCAGATCGAATTATGGAGAC
103	GCAGAGTCAATTATCATGCC
104	CGTTAGGCAATACATTTCCC
105	ACTGGTGCAAAGTCTTCGAC
106	GGTATATGAATGTGTCGTCC
107	GATAGTGCAATCTAGGTGAC
108	GCAGTGCAATGGATGTACTA
109	GCTAGGCTAATGTCCGGCTA
110	GGTAGCCTAATGTGTGCTCA
111	GGACGTGCAATCTTGTGACC
112	GAGCGCCGAATCTAGTCGAA
113	GGGAGCGACCTCTAGCTTAT
114	GCGGGTCGAATCTCGCTTAA
115	CGCCGCGCAAGCTGTATTAA
116	CGGCTGCGAAGCTGTCTTAA
117	CATCCGCTAAGATCGGTTAA
118	CGTGCGAGCATAATCCATCAG
119	TGAGAGCTGGATCGCATTCC
120	TAGGTGCTAGGATCTCAGCC
121	TAGGTATCAGGATTCAGGCC
122	TGCGCCAGTGAGTCGTATAT
123	CAGCAACGTGGATCAACTAT
124	CAGCGGCTAAGATCAATACC
125	GCAGCCTAATCTGGCCTAGT
126	GGGCCTGTACCTGCAATTCA
127	TAGGCCGGACCTGCTGTTAT
128	TAAGCCGCCACGGAGTGTTA
129	TAAGGCTCTTGAGACGTAGT
130	TAAGCCCGATCAGCATGGAC
131	TTGCCCGTAGTCAGCTTAGA
132	GAAGCACCGATCAGACACTG
133	CAGGCACCAAGTAGCACAGT
134	GGTGCGCCATGTACTCAGTT
135	TCAGGCTTATCGAGCGCGTT
136	GCAGGCAGATCGACCTAGTT
137	GGATAGGGACTCAGATATAC
138	GCATGGTTACCTACGCCAGA
139	GGAGGCTGACTCATACGCAA
140	GGAGCCTGACCTAGTCGATA
141	GCGGCCAATTCGGCGATAAT
142	GGTGCTCGACATTAGGCCAT
143	GATCCACATAGCGGACAAT
144	GATCCAATCTGTCAGCACAT
145	GAGCCAATCTGACTACCAGT
146	TGCTGGATATGACTGTCGTA
147	TGCTCTGCACTGCTGACGTA
148	TCACCAGCCAGACTGTGTAG

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Seq. Id	3' to 5' sequence
149	AGGAGCAACCATCATGCACG
150	GGGCATACCTATCCCGAGAT
151	CGGGCGATACCACTCAGATT
152	AGCGGCAACCAGACATACGT
153	CACGCCATACCAAGGAGAGT
154	CAGTGCATACCAAGCGACGA
155	CAGGCAGTACACAATCTACG
156	TACGTCGCATCCATAGCTGA
157	GAGTGACACCTCAGCAGATA
158	CTACAGCACCTCAGGAGAGT
159	CTCACGACATCCAGGAGTAT
160	CCAGCACGACAGAGAGATGT
161	CGCACACACCTGAGAGAGAT
162	GCGCACGCACTCAGATGTAA
163	AGACGCTCAACCACGAGAGT
164	GACGCCACAGTCACTAGAGA
165	GGCGCACACTGTACTCAGAT
166	CGAAGCGCCAGTACCAGATA
167	GGGTCGCTACCTACTCTGAT
168	GAGACATGATCTACCAGTAC
169	GGACGCTTACTCAGCAGTCA
170	CGGGTGTTACAGAGCTATCA
171	CGCGGCTTACACAGACATTA
172	CGGAGCTTACACATTAGCAG
173	CTGAGCATACACTTCACGAT
174	CCGATCATAACTGTAGATGC
175	CCGCCGATAACTGCTTGAGA
176	GGCCATATACGAGATGTAGA
177	CGTCCCTTAACGGCTGGTAT
178	ATACCCAGAACGACTATGCG
179	ATCCCACGAACGATGAATCT
180	ATCCGCAGAACCGGCGATAA
181	CCTCGCCGAAGCGTGTTTAA
182	GCGCCGCACAGAGTCTTATA
183	CGCGCTGCACAGAGCATATA
184	CCGCTGACACAGGCAGATAT
185	GCGTATGACCAGGTGTATAT
186	CTGTATGAAGGTGCTGTACT
187	GTTTCGCACGAGGATGTATC
188	GTGCTCGCAGAGGATTTATC
189	TAGGCCAGAGTAGCGACTTA
190	CAGATCCTAAGAGCAGTTAC
191	TAGATGCTAGGAGCGATTCA
192	TAAGTCGGTGGAGCATATCA
193	TAAGCGCGTGGACTCCTAAA
194	TAAGTGGACTGAGCGCATAT
195	TATACGGCAGTGGATCAGAT
196	CTATACGCAATGCACTCAGA

Attorney for Plaintiff, Defendant, and Intervenor

Seq. Id	3' to 5' sequence
197	CTATCGTCAAGTGATGGACC
198	TATAGACTAGGTGATCGAGC
199	TAGTACGAGTGGGCATCAAA
200	TAGACGTAGTGAGCATGACT
201	TGACGAGTTAGGATCTATGC
202	TTACGAGTGTAGCGTCCATG
203	TCGTCGTAGCATCTCGCAGT
204	TCGACGTAGGATCGCAGTAC
205	TCAGTATCATGGAGTACGAG
206	TGCACTAGATGGGATCGACT
207	TGCGATTACTGCCGTCACGT
208	TGGACTCTATGGCAGCCGTA
209	TGACAGCAGTTGCAGTCCGT
210	TACACAGGCTTGCAGCTCGA
211	TGCAGCGGAGTGCCTCATT
212	GCGCAGGGAGATCCATATCA
213	CGGCAGCCAAGTCCAGTATA
214	CAGCGCCCAAGACGTGTATA
215	GTGCCTGCATAGCGATAGTC
216	TGCCTGCGAGAGCCTGTATT
217	TGGCATCGAGAGCCGTTCTA
218	GCAGGAGCAGAGCTTATATC
219	GCGGGATCACGACGTTTACA
220	GTGGCGATAGAGCATTCTCC
221	AACGCGAGAAACCATTGCG
222	AGGCAGACAACCTCAATCCGG
223	AGGAGAGCAACCTACACTCG
224	AGCCAACGAACCTACATGGG
225	CCGCAAGCACGTCGAATGAA
226	GCGCATGGACGACAAACGTA
227	GCCAGGAGACGTAGATATTA
228	GCGCATAGAGAGAGATCATC
229	TGGTATATCGGTAGATTCGC
230	GAGCTATAAGGTGGATTCAC
231	CGCGGATAACTTGATTCACC
232	GTCGGCTTACCTGATAGCGA
233	GGAGCTATACATGCCTATCC
234	GGTGCCGTACATGCTCGTAT
235	TCGGCTTGACGTGCTCGTAT
236	GGGCTGTGACTAGACTCTCA
237	GCGAATTTAGTAGACGCACA
238	GAATCTCGAATAGCGGTACA
239	GACAGTTGACATGACAGTAG
240	GACATTGACATCGCATACAC
241	GAGTTTAGAATCGTGAGCAC
242	CTATTCGCAAGTGTCGAGCC
243	GTTATGGACACTGCTCGACG
244	AGCGTTCTAAATGCGTCACA





Seq. Id	3' to 5' sequence
293	GTTATCTACGGATCATGCGA
294	CTGCCGTAAGTCTCATGCGA
295	CTAGCCGAATACTGCATACA
296	CTGCCGTGAGAATCGCGTTA
297	CATACACGACAATAGCTTCG
298	GATACCGACTCATACATTGC
299	GATACCGCACGATCAGCAGA
300	GTATATGCAGACTACTGGAG
301	TATAGTCGATTATCCCAGCC
302	CATAGTACAATATCCCGACG
303	CTTGACAGCTACTACCA GTG
304	CTGAGACAGCTATCGACACA
305	CTGAGTAAGTCTTCCACACG
306	TCGGATATACTATGCGTCAG
307	CGTAGGATAGAATGCACAGT
308	CATGATACACACTCACGAGG
309	CGGAATCACGACTACATACG
310	GGGTATCACGAGTCACCTCA
311	GAGAGAATCGTATCACAGCC
312	GAGTATGTAATCTACCTGCC
313	GAGTAATCATAGTAGCAGCC
314	GACTATATCCAGCACCGAGG
315	GACATATAGCTCCACTCAGA
316	TAGACCTAGTTGCAGCGCGA
317	TACTACACGTTTCACGGCAG
318	GTACATATCTGTACGCGCA
319	TAGTATATCCTACGCCGCTA
320	GAGTATATCGCAATGCCAGC
321	GAGTTGTACATAGGCCACC
322	GACGCATGACATATTCCTAC
323	GAGACACTTGACAGTAGCCA
324	GGCTAGTTACTCAGATCACA
325	CGCAATAAGTCTAGCTCACT
326	CATGTACTAAGCAGTCACAC
327	CTAGTTAATGTCAATCCGCG
328	GACTGTGTAATCATTGCAGC
329	CGTTCGTGAATCAGCACAGC
330	ATTCGGTCACACAGCACAGA
331	ATCTGCTGACACACACTAAG
332	AGCTCGCTAAATATGTAGGC
333	ACTGTCTGCAAATATCACACG
334	ACTGTCTGACCAACCAATAG
335	GTTACTAGCTGGACCTCAGA
336	TTATAGACTGGTGCGGAACA
337	TTAGCATACTGTGCGCGAAC
338	TGTGCTGACTTAGGTCGAAT
339	TCTCGGGACGTTGCGCTATA
340	TGTCGCGACGTTGGCTATA

Attorney Work Product  
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Seq. Id	3' to 5' sequence
341	TGTTCTGACTGTGCGCTAC
342	TGTCAGGTACTGGTCGCTAC
343	TTTCATGTACTGTGGCTACCG
344	TTTACTAGAGTGGCGCATGA
345	TTAGATAGATGTTTCGGCCAG
346	CTCAATAGATTATAGGCGCG
347	TCGAATCGCTGTTACGGAAA
348	TCAGACTAGGGTAGCGCATA
349	TCAGCAGTATGTAGGCAGTA
350	TAAGCCGGGTACGCTATTT
351	TATGACCGATGTGCAGGTAT
352	TTAGCACGCTCGGCGATGTT
353	TTACACGGTCTGCGAGCTT
354	CTTCAGACAGGAGGAGATAT
355	TCCAGCCGACGTGCGATTTA
356	TCCAGCGTACCTGCTTGTAG
357	CTCCAGTCAAGTGCTTCGAG
358	CTCCAGCGAAGTGATGAGAA
359	TGTCAGCGGATCGCCATATA
360	TCCATGCGAGGATCAGGTAT
361	TGCAAGCAGTTCTCAGCGTA
362	TGTAGGACCTGTGCTCACTG
363	TTTATCGCAGTGCTCAGGCT
364	TATGTCAGCAGGCCAGCTT
365	TTCTCGTAGCTGCGCCTAGT
366	TATTCGAGCTAGGGACGCAT
367	TATTTATACTGCGAGCGAGG
368	GACCTTACACTGGCACGAGA
369	TACTGATAGCATGGGACGTT
370	TCGGATAGCAGTGCGCTCTA
371	GCTGATGCACGAGGCCATTA
372	GCTGGATCACGAGGCTCATA
373	CGCTTTGTACCAGGCCATAG
374	CGTGATTGACCAGACCCAGT
375	TACGCTGGATCAGACGGTCA
376	ATCCTGAACGCAGAGACACG
377	ATCGTTGCACCAGAACTACA
378	CTCTCAGGACCAGCATGATA
379	TCTGAGCGATCTGCCAGTCA
380	GGTGAGACCTATGTATATCG
381	TTAGAGTCTTAGGCATGTCG
382	TTATAGCCGTAGGCAGGTAC
383	CTCTAAGTATTGGACACGCA
384	GCTAGGATATAGGACACTGA
385	GCTATCGAATGTGCAGTACG
386	TCTATCCACTGCGGACGAGT
387	TCATACTCATGTGCAGCTCT
388	TCATCGAGATCGGCCACTGT



Seq. Id	3' to 5' sequence
437	CTTACGCCAAGTTGTCAGAA
438	CTTGCGTCAATAGTCTGAGA
439	CCTGTGCGAACTGTCTTACA
440	CTCAGTCCAAGTGGCTCAGA
441	CCATAGCGAAGCGCACAGTA
442	CCAGCACTAAGCGCAGATAG
443	CTCCGCCTAAGTGGCAGTAA
444	TGCGCCTGACGTTCCGATTA
445	TGTCCAGTAGCTTGAGAGTC
446	GCTCACAGAGTTTGATAGAC
447	GCTACAGGAGTGGATATTAC
448	GTGACAGTGGCAGATATAAC
449	TCGCACTGAGCTGTAATCGA
450	TCTTATGAGATGTAGCTCGC
451	TCCATCTAGCTGTAGCCGAA
452	GTCATAGCAGCTTAGACCTA
453	TTATGCTGACTGTGCTCGAC
454	TTAGTGCAGTATTAGTCGCG
455	TGTCTGACCTTGTAGCCGAC
456	TGTTGACACTTGCGTACCGG
457	TCTTAGCATGTGCGACGACG
458	GCTAAGCTCTTGCACTGACG
459	CATAAGACTTTCCAATCGCG
460	CTGAAGCACTTTCCACGAAG
461	CTGAACCCGTTGCAGAGAGA
462	CGGAACCGATGGCACAATAT
463	GGTGACCGATGGCTACTCAT
464	ATGGCGCGAACCCTGTACTA
465	CATCGCGGAAGCCACGTATA
466	GACGGCAGAATGCAGTATAT
467	CGCGGAAGAAAGCATATTTG
468	CTCAAGGGCACGCAATCTAG
469	TCACAGGAGGCTCGACTCTA
470	CGACAAGGCATTACACTAG
471	ATAAAGGTCATGCCAACCGC
472	TATAATGCGTTTCACGTCCC
473	TCTAATGCCTGACACGAAAC
474	TGAATGCCGTGACTCGTAAA
475	GTGGAGGCACTGCATCATAA
476	GTGGTGTGACCTCGCCATTA
477	GGAGATGCACTACGGAATAT
478	GAGGATCGAATACTGTCGTA
479	CGGAGAGCAAGTCATACGAC
480	GCAGGAGACGGAATATACTA
481	GAGCGTGTAAATCCGATCTAA
482	CGATACGGAAGGCGCACTAA
483	CGATAGGTAAGGCGACTCAA
484	GATGTGGCACGACGATCATA



אנו מודים לך על שיתוף הפעולה שלך.

Seq. Id	3' to 5' sequence
533	TACTGCGTACTCGGAGCATA
534	GCTCACGTACTCGACAGAAA
535	GTGTACTATGTAGCGAGATC
536	TAGTAGTACGCTGTCAGAGC
537	TGTCGTCGAGTCGTAGATAC
538	GTAGTACACGGAGTGATCCT
539	GTAGTACGAGCTGAGACTCT
540	GTGACTAGCTCGTAATTCTG
541	GAGACACGGTACTAGAGACT
542	CAACAGCGTCACAGACATGG
543	CTATGAGACCACCTCGATAT
544	ATTCGGCGACAACGCATTTA
545	GTTGCCGTACTAGGGATACT
546	GGCGCAGTACGATTGACTAT
547	GTGCGACGAGCTTGTCACTA
548	TGCGTGTGACTATTGATACG
549	CGTCTGCGAACTTTGCTACG
550	CTGTAGCGAAGTTCTCATAC
551	TCGGCGTTACGTGCTGACTA
552	TGAGCTATACTCGTCGTCAG
553	CCGATACTAAGCGTTACGAA
554	CGTCATACATAGGACTAGCA
555	CGCACGCTACAGACTATTAT
556	GCGAGCGTACTATACATAAC
557	GCGAGTCTACGACCTCTATA
558	CGGTACGCACGACAGTCATA
559	CGGTACATACGACTATACAG
560	CGCTAGATACACCACTGATA
561	CTCTAGGTACACTACTGCAT
562	CGTCAGAGACACTGGAATAG
563	CTGCGCGTACACTCGGATAT
564	CTGTCGCTACACTCGTGAGA
565	GTAGACGCCTAGTCAGATAG
566	GAGCGACTACGAGCCACTAT
567	GTGCGACTACGTGCATCACT
568	CGTAGGACACGAGCGTATAT
569	GGCGACGACGTGACTATACT
570	CGGTCACGACGACGAGATAT
571	GCGTCACACGAGCCGATATT
572	GTCGCTCACGATGCGGATTT
573	GACCGACAGATCGTGACATC
574	GACCACGTACATGAGCTGAC
575	GGCGACGTAGATGATATTCT
576	GAGACTGTAATCGCATATCC
577	GACTATGTAATCGAGCCTAC
578	GATAGTCGAATCGCGGATAA
579	TATACGGACTGCGCCCTAGA
580	TAGTCTAGCTGAGCCATCGA



Seq. Id	3' to 5' sequence
629	GAGCGATCACACGTCCGATT
630	GGTCGCATAGACGTATCAGT
631	GGTGTCTCACGAGTATCGAC
632	GTAGGCTAGACGGTCCACTA
633	GACGGACACTGAGCACATAG
634	GACACCTATGTAGCAATGAC
635	CACAGTACAATAGCACCTGG
636	CACCAGAACGTAGGCACAGT
637	CACTACTCAAGAGCCAGTTA
638	CGCCGACGAATAGCCAGATA
639	GCCGCACTACTAGCGATGAA
640	GACCAGTTACGAGCAGCGAA
641	GATCACGTAGGAGCACCGTA
642	GTACGCAGAGGAGTCATCCA
643	GTCGCTGACTAGGATCACGT
644	TACGCAGACTCGGACTCGAT
645	GTCGCTATATCGGACCTAAC
646	ACTCGCATAAACGACAGTCT
647	TGGAGTCGAGTAGTACATAC
648	TACGACATGGTAGGACGCTA
649	TGACTTCTACGTGGCGATAT
650	TACGCTCCGAGAGGCGATTT
651	CACCTTCGACGAGCAAGAGT
652	TACGCTCGCTCAGCTTAGGT
653	TACGGCATCGACGCTATTGC
654	TACGGCGACTGAGATGCCAT
655	TACGTGCTAGGAGATGTAAC
656	TATCGTCTATCAGATTGCCC
657	TATCGTATCCACGTTCCGAG
658	GATCGTACATCAGTGTCCAC
659	GAGTCTATATCAGTAGCGAC
660	GTTAGTCGATCAGTAGAGCA
661	GTCCTACGATGAGTGACGCA
662	CGTCTTCTAAGCGTGCTGAA
663	GTCTCCTACCGTGAGCAGTA
664	ATCTCACTACAAGAGCCTAG
665	CTGTGACGACCAGACGCTTA
666	CTGAGCGTAAGTGATTGTAC
667	CTCGTAGCAATAGATTTCCC
668	CTACGTGCAATAGCAGCTCA
669	CCGGCAGTACAGATAAGTCA
670	CGCCGGATACAGAGTAATCG
671	CTCAGCATACATAGTACAGC
672	CCGAGCTTACAACGTGTGCA
673	GACGCATTACCACTGGCGAT
674	CAGGGTGTACCACGAAGCAT
675	CGGTGTTTACAGCAATCCAT
676	CTGGCTGCAATAGCGCGATA





Attorney Docket No. 3108.1

Seq. Id	3' to 5' sequence
725	CACCTATGAAGAGACTCACG
726	AACTATATCAAAGCCCTGGC
727	ACAATACCAAATGCGCCGGG
728	AGAAACGCAAATGCCTCTCG
729	CGAAAGCATAATAGCGGTGC
730	GGCAGAATCTCGTGTACTAG
731	GGTACATTATGCTAGAGAGC
732	GATACATGATGATAGCAGCG
733	AGAACAGGAACATCGCTGCC
734	AGATAAGCAACATCCTGTCC
735	CATAAGCTAAGATCCTGGAC
736	ATTTAGCGAAGAAGCATGGC
737	ATAGCTCAATCAACGATGCG
738	TATATCGCATCCACTCTGGG
739	CATCTCCGAAGCACATTGAG
740	CATTGTCGAAGCACTTCAGA
741	CATTATCGAAGCACGGTACA
742	GATTCGGACAGCACGGCATA
743	GCTCCGGCAGTCACGATTAA
744	GACTGTCGAGCACCCATTGA
745	GATCGTCGAGCACGCCTAAT
746	GAGGTCAGACGACGCCTATA
747	GCGCGTATAGCTCTCCATAG
748	TAGCGAGTAGCACTTCGATA
749	CTAAGTGTAGCACCATCA
750	GTAGATCGAGCAGCCAGTCT
751	GACATAGACCATACCACGTT
752	CGTCTTCGAGCAAGTGCAGT
753	CTCTCCGGCAGCGATATGTA
754	CCCTCAGCACGAGATATAAG
755	CCCTTGCGAAGCATTGCGAA
756	CTCCAGGCAATGAGAGCACA
757	CCCAGATCAAGCGATGCAGA
758	CTGAATCCAATGTACGTGAC
759	CGGCATTCAAGGTAGCGACA
760	GCCCGATTAAGGTGTGTCAA
761	GCCCGATCAATGGCTGCATA
762	CGCCATCCAAGGGCTGTATA
763	CGGATGCCAAGGGCTTCATA
764	GGTTGCGCCAGGTCATCTTA
765	GGTCCGGCATGGATCACTAA
766	GGCTGGCACATGATCGTATA
767	TGGTTGCACTTGGATCGAAA
768	TGATTGCCACTGCTCATACG
769	TGTTGATCCATGTCCATAGC
770	TTAAGGCACTTGATCTCAGC
771	GTAATGCCCTGGACCGCAAT
772	GTAAAGCCTTCCACGGCAAT

Seq. Id	3' to 5' sequence
773	GTTGCGCCATTGAGCCAGAT
774	GTTGCCACCTGAGACGTTA
775	AATGCGCCACAAAGCGAGTG
776	CACCGGCCAAGAAGTACAGT
777	CATCCGCCAAGCAGAGTGAA
778	CGTTGCCAATGCACGAGCTA
779	GATGGCTGAATGACGTTTAC
780	GATTGCCTAATGAGTCTGAC
781	AATCAGCCAAAGATGTGGGC
782	AATCATGCACAAAGTTCGCC
783	ATTTAGGCAAGAAGCGCACC
784	AATTGGCTAAAGAGCGCACC
785	ACATTGGCAAAGCGAACTCC
786	AATGGGAGAAAGCCGACTCT
787	TGTGCTGGAGCTTCAGTCAC
788	GTTGTGCAGGATTATCGACA
789	GCTTGCAGACGAGTCATCAC
790	GGATGGATACTAGCGACTCC
791	GCTATGGCACAGGCATCTAC
792	GGACTGGCACATCCCGTATA
793	GGATCGGACCATTCTCACTA
794	GGATGGCGACATGCTCACTA
795	GAGCTGGCAATCGTCGTACT
796	GGATGGCTACATGATCTGAT
797	GGCAGCAATTCGGGCTAATA
798	GCCTAGCAATGTTCCCAGAG
799	GAGCGGCAATGATGATCCAT
800	TGGTGCATAGCTGCGATCCA
801	GGCTGCACAGGTGTATCCAA
802	GAGATGCCAATCGGCCATAA
803	TATATGGCACATCGTTGCGA
804	TGATGCCACGTCGTCTGAT
805	ATTGATCCACACACAGTACG
806	AGCTGATCCAAGCAACGTAC
807	GTTGATGCAGATCGCGTATC
808	TCGTGGGCAGATCGCTTCAT
809	TGTGGCCGAGATGCCTTCTA
810	TTTGCGGACTTCGCTATCAA
811	TCCCATGCACCTGAGTGGAT
812	TTTCATGGAGCTGTCGCGTA
813	TTTACCTGTGGTGATAGCGA
814	TTGTCATGCTGCCAGTCGA
815	CTTTCATGCAGGCAGAGCCA
816	CCTTTAAGCTGGCACACGAT
817	CCTATCAAGGATGCACACGA
818	CCGTCAGAATATGACACAC
819	TAGGTCAGATCATGCGCGAC
820	ATGTGCATACAAGCTACGAC

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Seq. Id	3' to 5' sequence
821	CTGAGAATATGAGAGACGCC
822	ACTCACGCAAATGAACGGCG
823	CTTAGCGAATATGCGATACG
824	ACTCTGATAAATCCGACACG
825	ACTGTGCGAAATCCCAGACA
826	ACTGATGTAAATCCACACCG
827	ACGTGAACAATTCCACACTG
828	ACTGCACGAAATCGACATCG
829	ACTTCTGTAAATCGCAGCAC
830	CTGTCTTGAATAGCGATCAC
831	ATGCGGTTAAGCGGTAATAC
832	TACGCTGAGTCATCCGAATA
833	CTTGTGAGACACTCCGACAT
834	CTGGTGACATACTATCAGAC
835	CGTGCGTTAAGCTGTCGATA
836	CGGTATCGAAGCTGTGCTAA
837	CGCGTGTGAAGCTGCCTATA
838	CCTAGTAGAAGCTCCACAGA
839	TGTGTGCGGAGTCGCCCATAT
840	TCTGTGCGAGGTAGGCCATAT
841	GCTGTGCGAGAGCGATCATCA
842	GCAGTCGGACGAGATTCTAC
843	GCGATGGTACTAGATCAGCA
844	GTGTAGGGACTCGTATCACT
845	GTACGAGCAGTTGAGCATAA
846	GTCAGTCGAGATTCAGCAGT
847	GTCGAGTCAGATGCACGTCA
848	GTGTATCTAGCTGCACGCAC
849	GTTGTCTTACGTGCAGTCAG
850	TATGTACTCGTATCGACGCA
851	TCGTGTGCGAGTATCCGCAA
852	GTACGTTGACAGTCTGCACA
853	TTCGTAGAGGTCTGCCAATT
854	ATTCTGAGAGACAAGCCTCC
855	ATTCTGACACAATCATCGCG
856	ATTCAGAACTAATGCACCGC
857	AGGTATGAACCATCGCACAC
858	ATTTGATGAACTCCGCAGAC
859	GTTTGCTGACCTCGCAGTCT
860	ATTGCCGGAACGCATTATAC
861	TGTGTGGGATCGCCCTATCT
862	TTGAGTGAGCTGCGCTTATA
863	TGCGTGCAGGTGCCACTAAA
864	GTGCTGCATGAGCCAGTTCA
865	GGCTCTACATGGCGATAGCA
866	GCTCTCTAATTGCGGACACA
867	GGATATAAGTTGCGGCACTA
868	GGATGTAATGGTAGCTCCTA

Attorney Docket No. 3108.1

Seq. Id	3' to 5' sequence
869	GGATGACGAGGTCTCACCAT
870	GGATGCGACGATCTCGACAT
871	CGTGATCGAAGGCTGCACAA
872	CTAGATGTAAGTAGCTGGAC
873	CGAATGAAGGATCGAGACCT
874	CGGCCTGGAAGTCACTCATA
875	GGCCTTGGACTACCGCTTAA
876	TGCTTCGAGGGTCCCACTTA
877	TGCCTGGTACTGTCCGACTA
878	TGCTTGTGAGAGTCGCTACT
879	ATGCTTGCAGAACCGTCAGC
880	TGACTGTAGGGAGCCTCAAC
881	TGCTTGGCAGGATGTCTTAA
882	GGCTCCGGCATGAGTATATC
883	TGCTTTGCAGTGAGGCTCTC
884	CAATTTGGAAGTAGCCTTCG
885	TTTGCTGCATCCGGCCTGTA
886	TTGGGCCACTGCGCTCTTTA
887	TGTGAGCCCTTGGCACGTTA
888	GGTGGCCCGATCACATTCAA
889	GGCAGGGCACCTCAGTTTAT
890	GGGTGGCCCATGCTATCTAA
891	GTCTGGCCCTACCTATGGTT
892	GCGGGCACACCTCTGATTTA
893	GCGGGCGCACCATTCAATTAT
894	GGAGCCCACCATGAGCTATA
895	GAATCTCCACCAGGCGGATA
896	GGATACGTCGCTACAGTGAT
897	TCGTATAGCTGTATCGACGG
898	CTAACTAGCTGTAAGCGACC
899	ACTAGATAACAGATGCGCCG
900	CAACTATCATCAAGACGGCG
901	CAACAGAGATGAAGCGCGTC
902	CAACATATCATAAGCGCGTC
903	GCAGATAGCATCATATACGC
904	GCAGACTGAATTAGCTCTAC
905	GTTAATTCATCTAGCGCGAC
906	AGGAATCTAACCACGCGCAG
907	AGACCAATAAGCACCTGGG
908	AGACAAACATTACGCCGGG
909	AGAATAAATTACTGCCCGGC
910	GAGCACATATTATTACGCC
911	CAGAAGATAATATGCTCGCC
912	GAATAGCCGATAATCTCAGC
913	GAATAGCTTTACACTGCCCT
914	GAATCACTCTGAATGAGCAC
915	GGATCACACTGCCGGACTAT
916	GGACCCATAGCACTCTGATT

Seq. Id	3' to 5' sequence
917	GAGGCATTAGCACCAGCTCT
918	GGATTATCAGCACTCAGTAC
919	GGGATCTCAGACGATGCTCT
920	GGGTATATCAGCGGATTCCA
921	GCAATTCGATCTAATGCTCC
922	ACCAATGCAAATAGGCGGCC
923	AGCAAATTAACACTTGGGCC
924	GAAACAAGCAGATTTGCGGC
925	TTAATTCCGTGATATGCGCG
926	GGATCTAATGGTTATGACCG
927	GCATGAAGTGGTGTCAACTC
928	GCTTTAATGGTCGTGACGCC
929	GCTTAGAATTTAGTGCAGGC
930	GCGTCAGAATTTATGCCACA
931	GCTAGATAATTTAGGCCACG
932	GCTGATAATGCTGAGGACTA
933	GCAGAATTGCATAGACGCAC
934	GCATGATTAGCATAGACGGA
935	CCAGCAATAGCAATCACGGG
936	ATTGCACATTCAACTGACGC
937	TGGCATTTACTTAGTGCGAC
938	GAAGCCATATCAATGCTCAC
939	GCGAGCAATTTATGCCACT
940	GGCCCAAGTTTGTGACATGA
941	GGGCATAATGGTTGATACTC
942	TTGGTGCATGGATCTCTCCC
943	TTTAGGGCAGGTTAGCTTCC
944	TTATCCGGCTAGAGTGCGTC
945	TGATGACCTGTTAGCAGTAC
946	GGACCATGTGCTACGCAAAT
947	GTGAGCAGATTCAGCCAGAC
948	GAGAGACCATGCAGCCGATA
949	GCGTCGTCAATGTTGCCACT
950	GGGTTAATCCCTGCCACGTA
951	GTGCTGACATTGCGGCCATT
952	GCCTGTAATCGTGGGCACAT
953	AGCGCGTGAAATGCACATAC
954	AGCGTCTGAAATGCTATCAC
955	AGTGCGCGAAATGTTCTACA
956	CGTCGCCAATATGATCGAAT
957	CGCCACAAGTTGAGCGATA
958	GCCCTACAGCGTGAGCTATA
959	TGTCAGTGATCCGGGACTAT
960	GTTATCGCACCTGAGGCGTA
961	GTTGTGACCTCTGAGCACGT
962	GTTTCACGCTATGCGAGCCA
963	GTTTACCGCTCTCCAGGGAT
964	TGCGTACCTCCTGCATGGTT

Attorney Docket No. 3108.1

Seq. Id	3' to 5' sequence
965	TGACTACCGTGTTCGCATACG
966	TGGACTACGTGTCTCGATAG
967	TAGTGATACTGACTCATGGC
968	CGTCTGATACAGCCCAGTGT
969	GCCGTATCACGACGCTAGAT
970	AGCTCGATACAACGCTAGAG
971	ATCTACTTAACGCGCTACAG
972	GACATCGTACCACTGCGTAG
973	GA CTCGTGACCACTCTGTAG
974	GA CTCGGACCATATCTACGG
975	CACTACGCAAGACTATGTAC
976	CGAGTCTCACAGCAATCTAG
977	CGATCTAGCACGCAATATAC
978	GACCAGCGACGACAGTAGAT
979	CGTAGACAGCCACGCAGTTA
980	CGTATGCTACCACCGATTAT
981	CGTGCGATACCAGCGTAGAT
982	CTCCGTACAGCAGGCAGTAT
983	CTCGTCGTACAGCGATCAGT
984	CTACAGATACGTGAGAGAG
985	CTACGCGACACGCATGAGAT
986	TAGACGCTCGCACGGTAGTA
987	GCCGCTAGACGACGGTATAT
988	GTATCACTAGGACGAGGTAT
989	GTA CTCACAGTGCGAGAGCT
990	CGACTACACAGCTCAGGATA
991	CACCGACAACCTCGTAGAGAG
992	CGACCCACACTAGGAGAGAT
993	ACGCGCACAAACAGGAGACTT
994	AGTACCACAACCTCAGACGTG
995	AGTACAGCAACGCAGAGCCT
996	GTCAGCGACCGTCAGCTATT
997	GTCAGGCACTAGGAGCTATC
998	TGTCGGTCACTCCTGGACTA
999	TCGGTTCACGTCCGCATGTA
1000	TCGTTTACCTGTCGCGCTGA
1001	TGTGTCTCACTTCCGCGAGT
1002	TCTGAGCACTCTCTCGTAGG
1003	GTTGATGACTCGCCACACGT
1004	CTGAGATCACAGCAGACTAG
1005	TTAGACTCCTCGCCGGTAGA
1006	TATAGCTCCTAGCAGGCGTA
1007	TATGCTCCACGTCTAGTGAG
1008	CTCTATCACCAGCGATGAGA
1009	CGCTCCAGACAGCATATAGA
1010	ACATACCGAAAGCTCTAGCG
1011	ACATCGCTAAAGCACATCGG
1012	ATATCGCGCAATCAACGCTA

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Seq. Id	3' to 5' sequence
1013	CGATGCGCCACTCAAGGTAT
1014	TATGCCGACGGTCAGGCTAA
1015	TATCGCCACGTCCGGTGATT
1016	TCTCGCTCACTGCGTATGAT
1017	TATCCGTCACTCCGTAGAGG
1018	TATCGACTATCCCTGAGACG
1019	GTATAGACCTCTCAGACGCG
1020	CTATCGTAATATCAGTCCGC
1021	CGATGACAATTAGGTACACG
1022	GAGCATAATGACGTAGACCG
1023	CGACAATACTTGACAGCACG
1024	CGATGATAATAGAGTAGCCG
1025	CTATGATTAAGTCGTAGCCC
1026	AGGTGAATAACGCATACGCC
1027	GAGTGAGTAATGCTACGTCA
1028	GATCGACGAATGTTAGAGAC
1029	GA CT CACGAATGCGGAGACT
1030	GACCGTCAATCGCGTCAGAT
1031	TACCCGCATCGACGGAGTTT
1032	GTCAGCGCACTCCTGGTTTA
1033	TCAGGCCACGTAGCGTTAT
1034	TTGCGGCTATCCATGCGTGA
1035	TGCTGATACTCGGCTGCATC
1036	TGAGTAGCATCGGTGACTTC
1037	TTGTATCACTGTGCTGCCCA
1038	TTTAGTCAGTATGCTCGCGG
1039	TTACGTTTATATGGCCGAGG
1040	TGAGATCACGTTGCGCGAGT
1041	GTATCATTAGCTCCGCAGAG
1042	TATCATGTAGACTCGGAGGC
1043	GTATGCTTAGATATGCAGCG
1044	TTGTAGTTAGCTCTGCACGG
1045	ATATCGTTAAGCCATACGCC
1046	ATTCTGATAACGCTCTCGAC
1047	ATTCGTCCAACGCGGTCGAT
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1053	ATGTGTTCAACGGAGACAGA
1054	CTCTTTCTAAGTGAGTCGAG
1055	CTGCTTGAAGTCGTCTCACG
1056	CTGCGTTGAAGTGGCTTACT
1057	GTGCGTTCACATGGCCGTAT
1058	GTAGCCGCACCTGACTGTAT
1059	GTAGCGCCACCTGACGTTAT
1060	GGCGCGTCACATGATACATT





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Seq. Id	3' to 5' sequence
1109	CCCAGGGCAAGCGATCATAA
1110	GCCACAGGCAGGGCATATTA
1111	GCCTAATCCTGGGACACTGA
1112	TCGTCTCGATCTAGGCCATG
1113	GTGTCTCGACTCAGCCTATA
1114	GACGTAGTAATCATGTCTCC
1115	GACTIONACGTCATGCGACC
1116	ACGATGTAACACAGCGACCG
1117	AGTCGTGTAACCATGTGACA
1118	GTCGTGACAGTGATGTACTC
1119	GTGGAGTGACGTATCTCTAA
1120	TAGAGGTGACGTAGTCCACT
1121	GTCGTGCGAGATAGCTCTTA
1122	GTGTAGAGATATAGCATCGC
1123	TAGTCGTGAGATAGCGATTCT
1124	CAGTGTGTACGAATACGAAG
1125	CGAGTGTCACATACCACATA
1126	CGTATAGCAGACAGCGCAAT
1127	GACATCGACGACAGGCCATA
1128	CGAAGCTCACGTAAGTCAAG
1129	TAGTGCTCACGTAGCCCAGT
1130	TGCCCACGGTGAGCTAGTTT
1131	TAGCTGCCAGGAGCGTTCTA
1132	TCGGCCTACGCTGTGCATTA
1133	TAGGGTACTGATGAGCACTC
1134	CTACGGGAAGGTTAGCACCA
1135	TGGTGATACCTGTGCGCCTA
1136	GATTAGATACCACTGCCACA
1137	GGAGTGATACCTCGATCCAC
1138	AGCTGACGAAATCTTCACAC
1139	GAGGAGATAATGGTCACTAC
1140	CACGGAATAATACATCCTCG
1141	ACAGCAACAAGTCGAGCCGT
1142	ACGGAGAGAAATCAGCCCTC
1143	CAAGAGATAATACGGCTGCC
1144	CAAGTCCTAAGACAGCTACG
1145	ATAAGCGCAAGACAGGCGTC
1146	ATCTGAGCACAACTAGGACG
1147	CACAGGCTAAGACAGGAGCT
1148	CATAGCGTAAGCCAAGCAGC
1149	CATAGTCTAAGCCACATCAG
1150	GACAGTACATGCCAATCAGC
1151	GCGGTAATCGGTGCATCAAA
1152	GGGAGTATAGCTGACCATCA
1153	GTAGGCAGACCTGATCCCTT
1154	GAGCCAGACCACGCTTGATT
1155	GGCGCATCACTAGCCAGATT
1156	GGAGCTACATCCGCCAGTTT

Attorney Docket No. 3108.1

Seq. Id	3' to 5' sequence
1157	GGAGTCTACCCAGGGCATT
1158	CGCGCTCTACACGATGGATA
1159	CGTGCCACACCTTGGAGTAT
1160	CGCGGCACACAGTTCAGTAT
1161	GCTCGTCCACAGTGCGTTAT
1162	GCTGACGCAGAGTCCAGTTA
1163	CCGTAGCGACAATCAGCTTA
1164	ACGCACCGAAAGTGAGCGAT
1165	ACGTCCTCAAAGTGCAGACA
1166	ACGCAGTCAAAGTCATATCC
1167	CAGAGTCTAAGATCACCACG
1168	CACTGTCTAAGATACACACG
1169	CAGCGTACAAGCTATACAGC
1170	CCGACGACAATGTACGACAG
1171	GA CTAGCGAATCTAATGAGC
1172	CGTCGAGCAATATGAATGAC
1173	CTGTGCGCGACTTCATAGGA
1174	CCGCGACCACGATAGAGAAT
1175	GGCACACACGTCTCGGATAA
1176	GGCAGACGACGTTGCATACA
1177	CGTGGGACACAGTCGATCAT
1178	AGTGCGAGAACATCGTGTA
1179	GGCAGCACAGCTTGTACGAT
1180	GACCATTGAATATGTCGAGC
1181	GTACGCATATTTAGCCAGCA
1182	GGCAATCTGTTACGACCAA
1183	GCTGACTAATTGCTAGACAG
1184	GGTGTCTAATTGTATGCACG
1185	GTTGACACATTGTTAGCAGC
1186	TTAAGAGATTAGTCTGCCGC
1187	TCACGTAATTTGTTAGCCGC
1188	TGAGTGATAGCTCGGATCTC
1189	ATGATGATAACTACGTGCCC
1190	ATGCGAATAACTATGACGCC
1191	ATGGAGATAACTATGCACCC
1192	TCGTTGCGACCTATGCGTAG
1193	TAGTTCGCACCTACTGCTAG
1194	ATACGTGCAACCACTGCTAA
1195	ATGTCGATAACCTCTGCTAC
1196	ATCTAGTCAACCTGAGCTAC
1197	AGTATAGCAACCTCAACTCG
1198	AAGACACTAACTCTGCTCG
1199	ACGATAATAACAGCTCCTCG
1200	ATAGATATAACTGACGCGCC
1201	ACTGTAATAACCAAGCCTCG
1202	ACTGATAGAACCACAGCGCG
1203	ATGGCGACACACATACAGCG
1204	ACGGCGAGAAATACGATGCC



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Seq. Id	3' to 5' sequence
1253	AACCTAGCAAACCTTAGCGCC
1254	TCTTCGATATGATAGCGTCG
1255	GACGTTAATTGATGAGACGC
1256	GCGTGAAGTTGTTAGCACAT
1257	GCCGATACATGCTGCACGAT
1258	CGCCGATTAAGCTGCGACAT
1259	CGTCATTTAAGTTAGCGCAC
1260	CTCCATCTAAGGTGCGATAC
1261	CGCTTATCAAGGTGCAGACC
1262	GATGACTCAATGTGACTCAG
1263	CGCTAGTGACAATTATGTGC
1264	GCTAGGTGACAGTATGCTAT
1265	GCTGTGCTACGACGTTGACA
1266	GCTAGAGTAGACCGATGCCA
1267	GTATATCGAGATCATAGGCG
1268	GTCTTGGA CTATACGAGCGC
1269	TACTTGTAGATAGCGAGCGA
1270	GTA CTCTGACATGATTCGCA
1271	TATACTGACCTTATCGGCAC
1272	TCGTCTTGAGATATGTGGAC
1273	TCATGTTACGGTATGCGAGA
1274	TCATCTGCACGTATCGTCAA
1275	GCGACTGGACAGATTGCATA
1276	CGGGCGCGAAGTATTCACAT
1277	GTGTGGGCACGTATTCCATA
1278	TCCGGGCACGGTGT CATATA
1279	TGGGCGCTACTGGCTCTTAA
1280	TGCGCCGCCAGTCTGTTATA
1281	TGGCCGTTAGAGTCTGCACT
1282	ATGGGCGCAACCCTGTCATA
1283	CAGCCCTGAAGACTGCGATA
1284	CGCCGCTCAAGGCTATGATA
1285	CGCTCCTGAAGGGTAGTTAA
1286	GGCCCGACAGGTGCTATTAT
1287	GGATAGGCAGATGCACTTAT
1288	GGACAGACGTTGACCAGCTA
1289	GTAGCGACATTGAGTTAGCA
1290	GACTACGAATTGAGCATACG
1291	CTACACTAATTGCAGCAGCA
1292	CGTACCCGAATGCAGCAGAA
1293	GACGCCTAATGACGCTGAAA
1294	TAGCTTGTA CTGCGACTGAC
1295	GATACTCTAATGCCATCGAC
1296	CGGCGTACAATGCCATAGAA
1297	CGGATACGAAGGCTATGCAA
1298	ACGGATCGAAAGGTATAGCC
1299	ACGGCGCGAAAGCGTCATAA
1300	CGTGAGGGAATACGTCATCA

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Seq. Id	3' to 5' sequence
1301	CACAGTGAAGACGCATCAC
1302	GAGGTGACATGACGTACATC
1303	GAGTAGCGAATGCTCAGCCA
1304	TATAGCACAGTGTCCAGCAA
1305	CGTATGTCAAGGGCCTGATA
1306	CGAGACGCAAGGGATTACACA
1307	GAGACGCAATGTGAATTACG
1308	GATCGCACAGGAGCGTATCA
1309	TGCCCAGAGCGTATGAGCAA
1310	TGAGGGCGAGCTATCTATCA
1311	TTGTGGCTAGGTATCGCTAC
1312	TGGTTAGCAGGTATGATCCT
1313	CTCACTGCAAGGATGGGACT
1314	TCCTGTAGATCCCTATGCGG
1315	TCGTTGTCAGCATATTGAGC
1316	ATCATGTGAACCTATTGGCC
1317	TACACTGGGACCTATGGGCA
1318	TACCTGGGAGCATAGCTGAC
1319	TAGCCCGCAGCATAGGGTAT
1320	GAGCCTCAATGCTACGGAAG
1321	GATGTTCAATGCTGGCCGAA
1322	GACTTGTGAATATCTGTGCC
1323	GCCGCCGAATTATTGAGCAA
1324	TGGACTGATTGATAGGCAAC
1325	TGGCAGATCGGTGTATTCAA
1326	TATGCGTAATGGGTGTTCCA
1327	TTAGGTCGATTGATAGTCGC
1328	TCTGCTTTACTGCGTAGCCA
1329	TTGACGAGTTTGCAGTGCTC
1330	CTTGATTAAGTGCTGTACGC
1331	CTCGGATCAAGGCTTACCGT
1332	CCGGGCTCAACGCTTTGTAA
1333	TGTCGCCCAGCTCATGTGTT
1334	CTGGACCCACAGCTATGGAT
1335	CACGGGCCAAGAGATATACC
1336	CGCCCGCCAAGTGATGTATA
1337	CGCCAGCCACATGGATAGAT
1338	GCCCGGATACATGCGATTAG
1339	GCTGGCCTACATCCGTATGA
1340	AGATGGCGAAATCCGTATAG
1341	GCAGGGACATTACGATCAGT
1342	AGCAGGTGAAATCGTACTAC
1343	GCAGGTCAATCTCTGTACGA
1344	GCATTGTAAGTTCGGTCAAG
1345	GCACTGGTAATTCAGCTACG
1346	AGCATCATAACCCAAGCTGG
1347	ACCAGTCCAAAGCATAGTCG
1348	ATCATTTCAACGCAGTGACC

Seq. Id	3' to 5' sequence
1349	TCAGCCCTATCGCAGGATGT
1350	GTCAGCACCAGCCGTGATTA
1351	GAATTACGCACCCAGCTTGA
1352	GAATGCGCCTACCAGCTATA
1353	GAATGGCGACAGCGTACATA
1354	GGATTGCCACGACTCACAAA
1355	GCTCATTGACACTGCGCTAT
1356	GAGCATGGACCACGGCTATA
1357	CAAATGGACAGACAGCCTGC
1358	CACTTTGAAGCACAAACACG
1359	GCTGTTGCAGGACGCATCTA
1360	TACCTGGCATGACGCGATAT
1361	TTCGTGGACTTGCGGATCTA
1362	TTCTTGCGATAGCGGCGTTT
1363	TTGATCTGATAGCGGGTCTC
1364	TTGATCGCATAGCGTCTGAC
1365	TTCGAGGCATGTGGATCTCC
1366	TTCAGCGGCTAGGCGATTTC
1367	TCCAGCAGATCGGCGAGTTT
1368	TTCAGCCGATCTGCCGATAT
1369	TTCTATCGCATGTCAGCCGT
1370	TGTAATGCCTGCCAGCCGTA
1371	TAATTGCCTGCACAACCTGGA
1372	TAATTCCATTGACGGCAGCG
1373	TTATTGCCATAGCGCGACGC
1374	ACAATTTCAAAGCCTGACCG
1375	ACAGGCCCAAAGCACTAGGT
1376	CGAATGCCAAGGCCAGCTAA
1377	GATGGTTCAATGCCTGGACA
1378	CTGGGCCAAGTTCTGAGACA
1379	CGTGGGCAATACAGTTGAAT
1380	GAGCTGCGAATCGGTATTAA
1381	GACCGGCGAATCGAGCATAA
1382	GACTTCGCAATCGGCACGTA
1383	GACGCGCCAATCGTGCTATA
1384	GATCGCTGAATCGTGCGTAA
1385	GATCACTGAATGCGACGTAA
1386	GATCGTGCAATGAGGTTACA
1387	GAGGACTAATTGAGATGCAC
1388	GACCGATAATTCGATATGCC
1389	TAGCATTGATCCCATGTCAC
1390	TTCAGCTTATGCCAGTCGCG
1391	TGACGGCCTTGATATCCGA
1392	GAACGCGCCTTACATCAAGA
1393	GAATACCAGTTACACTCCAG
1394	CAAGAACTGTTACACATCGC
1395	GACGAGAATGGACTACACGT
1396	TACAGACGCTTGATAGATC

Seq. Id	3' to 5' sequence
1397	TAACGACCTTAGCGACGGGT
1398	TAACGACGCTTTCCCAAGGA
1399	TTACCGCTGTTGAGCCCGTA
1400	TTCCATGTATCGAGCGTCAG
1401	TATACGCCCTTCAGATCGGG
1402	CTAAGCCTATGCAATATCGC
1403	CCAGCTATAAGCATATTGCC
1404	TACAGCATTGTCATGGACTC
1405	TAAGCTATTGGACATTGGGC
1406	TTAGCATCCTGTCATAGGGC
1407	TCTAGCAGCTTTCATAGCCA
1408	TCATCACGCTTCCGAGGAT
1409	GCATACATTGGACGAGAGCT
1410	TCTAGCATTTAGCATGGTGC
1411	TTATGACTTGATCTGAGGCG
1412	TGTTCGCACTGGCTTAGCTC
1413	GAGTTGAATGCAGATAGCTC
1414	TGCAGGCTCGCAGATGCTAT
1415	TGCGAGGACTGTAGCTTAAT
1416	TGGGCACTCTCGCCTAGTTT
1417	TGAAGCGCCTCGACTAGGTT
1418	TCATCGGCACTGATAGCTCA
1419	TCATCAGGCATGGAGCCAGT
1420	TAATCAGCGTTACGTCCGCA
1421	GAATGTGACGCAAGTCTGAC
1422	AGATTTGCACAGATAACGCG
1423	GATTACTGACCAGCATCGAG
1424	AACTATCGAAACCGCCAGGG
1425	ATAATACAAGAGTCGCGCCG
1426	ATAATCATAACCTCGACGCG
1427	ATTATCATAAAGGCAGGCG
1428	TATATCGGATCAGCAGGTCA
1429	TAATTTGCTACGCAGGGAG
1430	TAATCCTGTTACGCGGAGGC
1431	CTTTAGCTCCACGCAGTGTG
1432	TTCTAGCCGTCCGCAGTTTG
1433	GTCATGCGAGCAGCAGTCTT
1434	GGCGTTCGAGCAGTCATCTT
1435	TACCGCCAGTCAGCGAGTTA
1436	TACCGCCTAGCAGCATTGGT
1437	TACCGCACTGCATGTCAGGT
1438	TGTCTCGATGCAGGTCTAGT
1439	GCCGCATGACGAGGATATAC
1440	TACCGCGAGGCAGGATTCTT
1441	TACAGCAGTGCAGGGCCTTA
1442	GCAGCTAGAGCAGAGTATCA
1443	GACAGCAGATCAGAGACTCC
1444	TAAGCACGTTTAGAGCTGAC



4

Seq. Id	3' to 5' sequence
1445	TAACCGTGTGCAGATCGGAT
1446	TACTGCGGACCTGGATCTAC
1447	TCAGGGCTACTCGATTGGAA
1448	TCCGCAGACTTAGCGTTACG
1449	TGAGCAGCCTACGTTACTAG
1450	TGCGTCAGATGCGTATATGC
1451	TCGTCCAGATGCGGAGTTCA
1452	TCGGCTATATGCCAGATCCT
1453	AAGGACAAAGAGCGCGTCTC
1454	TAGCACCGATGGCGAGCTTA
1455	TGTCCACGGTGCCGCAATAT
1456	TGGTCCGACTGCTGCTACTA
1457	TGTGCCGACTGCCGTCTTAT
1458	TTCGCAGTATGGATCGGTAT
1459	TTACGCAGTTGCATGGAGCT
1460	TTCTGATTAGCTGCGGACGC
1461	TGGTTATACTTTGCGAGAGC
1462	TTTGTTAGCTTCGGGCAGCC
1463	TTGGTCTGATCCGGGCATAC
1464	TGCTTGGACTCCGGCGATTA
1465	CTGCTTGGACCAGCCAGTTA
1466	AAGCTGGGAAACGCACACCT
1467	AAGCGGGCAAACGATATGCT
1468	AAATGCCGAAACCATCTCGT
1469	CCATTCGGAAGCGACTCGAT
1470	TACATGGGCTGAGAACGCAA
1471	TATTGGGCGACGAGCGCCTAT
1472	CATCCGGGAAGAGTAGCACA
1473	ATTTTCATGCACATAGCACGC
1474	ATTGCAGCACAAGCCAGACT
1475	TTGCTAGGCTCAGTCCCGAT
1476	TTGGCGAGCTGCGTTCTCAT
1477	TCCAGAGATGCGACTGCTA
1478	TTCGCTGGATCGGCATGTCT
1479	TTGCTCCTAGCTCGCGTGAT
1480	TTGCTGCTAGTCCAGTAGGC
1481	CATTAAGCAGTCGAGAGACC
1482	CGTTAATGCAGCGAGAATCA
1483	CGCAAGCTCAGCAGAATTAC
1484	CCATGTCGAAGCATTTCATAC
1485	CTGAATGTAATCATCGTGCC
1486	CTTAGATGAATCACTGCCAC
1487	CTTCACGGAATCTAGGCACA
1488	CACTCTTGAAGCTAAGCACA
1489	CCTCTAAGCATGTTGACACA
1490	CATGCCGGAAGATGCGTACA
1491	CAGGCAGCAAGATGTACGAC
1492	CAGTGGGCAAGATAAGATTC

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Seq. Id	3' to 5' sequence
1493	CCGTGCCCAAGCTAGTGATA
1494	GATCGGGCAATCTGCGTACT
1495	TTCAGTGCATTATAGTGCGG
1496	TTATCTGCATGAGTAGGTCG
1497	TCGATAATCTTTGTAGCGCG
1498	TCTTACAGCTTTGCAGGGAG
1499	TCCTACATTTGCCACGGGAG
1500	TCTTCATCAGTGAGGCGCGA
1501	TTTCTAGGATGTATGCGAGC
1502	TATCCAGCATTACTGCGAGA
1503	TTATTCTCAGCACGCACGGA
1504	TGATTCGCACTCGCGGCTAA
1505	TTTGTATGAGTCGCTCCGAA
1506	TTCCGATCAGTCGATGCAAA
1507	GATCGTCAATCTGATGCACC
1508	AGATCGCTAAATGAGGACCC
1509	GATGCTATAATCGTATGGCC
1510	AGGAGCGTAAATTATCAGCC
1511	GGGCGATGACTATATCTGAA
1512	CTGGATTGACACTAGCATAC
1513	CTGCGGATACCATAGACAAC
1514	ACTGCAATAACATATCCGCG
1515	AATGACATAAAGTGCTGCCC
1516	ACATGCAGAAAGTAGTCCGC
1517	ACAGGCGAACAATGTACCCG
1518	ACCAGCACAAAGTCTACTGT
1519	AGAGAGCCAAATGACTGTCC
1520	TAGTGCATAATTGCTTGCCC
1521	TGAGCATATAGTATTCGGGC
1522	TGAGCGTTAGAGCTTGATCC
1523	TAGGCGCTAGGACTCGTTAT
1524	TATGGCCGACGATGTGTCAC
1525	TATGGCTGACGTAGCGCACT
1526	TCTCGGTTACTGAGTGGACT
1527	ATAACGGGACAGAAGCTGCT
1528	ATAGAACTCAATAGCCGCTC
1529	CATAATACACATACGCTGCG
1530	CAGTACGCAAGCAGATAGCC
1531	CAGACGCGAAGATAAGTTCC
1532	CAGCCAAGATAGCATACTCG
1533	TCCCATAGATAGCTCGCTGG
1534	TTCGCATGAGTGCTGAGTAC
1535	TTCCATATACTGGTCGGCAG
1536	TTTATGATATGCGTCGCGGA
1537	TTTCTTATATGCGCGAGCGG
1538	TGTTGCATATTAGCGGCTCG
1539	TATATGACATCTCTTGCCCG
1540	TTGTCCACATTTGCGCTCCGA

Seq. Id	3' to 5' sequence
1541	GCATCCGAATTGCGACGACT
1542	GGATCTGAATTGCGCGACCA
1543	GGCTATGAATTTGCGATCAC
1544	GGATATGCAATTTGTAGCCC
1545	CAGCGTATAGCAAGATGGAT
1546	CGAGCGATAATCAAGTCGAG
1547	CGCGGATGACACATACTCAG
1548	CGACGAGCACCAATTCGAGA
1549	CCGTAGTGACCAATGCAGAC
1550	GCGATATACATCATTCCGAC
1551	GACAGTCTAATCACTCGTAC
1552	GCAGTTATACTAAGGTGTGC
1553	GCAGTAGTAATGAGTGTCAC
1554	GCAATGTAGTCGAAGTGCT
1555	GCATATAGATACCATTGCG
1556	CGAATACTAGACACATTGCG
1557	CAACTACAGTACACAGCGTG
1558	AGACACAGAACTACCGCGTG
1559	ATAGCACAACGTAGACGCCG
1560	ATACAGTCAACTACATCGCG
1561	AGTACAACCTAGAATCCGGC
1562	GAAGACTACTAGATACGCGC
1563	CGATAATACTACAGACTCCG
1564	CCGTGCGTACACATAGATCA
1565	CGTGAGCGACACATGATCCT
1566	CTGTAGTGACATATAGAGCG
1567	ATGTCGTCACACAGAATACG
1568	ATGCTACGAACTACCAATCG
1569	ATGATAACGTACACACCTGC
1570	TCGGTCTACGTCTGCTCAGT
1571	GGCTCACGATCCACTGGTTA
1572	TGCCTGATACCTTGGATGAC
1573	GGCCGTGAATTATCATAGAC
1574	GGCTTGGACGCATTGATAAC
1575	CCCATCGAAGCATGTGTAAA
1576	CGGCATCGAAGGCGTTCATA
1577	GCCAGTTGACCACTTCTGAG
1578	TCGCATTAGCCATGTGGAGC
1579	GCAATCTAGTCTAATGGCGC
1580	CTAAGATGTTCTAATCGCCC
1581	CCAATAGTAAGTAATGGGCC
1582	TCATTATACTCTGATGGCCC
1583	ATGCTAATAACTGATCGCCC
1584	AGTGTCAACCATGATGAACC
1585	AGAGCATAACATCATGGCCC
1586	AGAATCTAACAGCGATGCCG
1587	ATTTAGACAAGTCGATGGCC
1588	ATATTAAGAAGTAGGCGGCC

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Seq. Id	3' to 5' sequence
1589	CATATCAGAATACGATGGCC
1590	GATATACAGGATTATGGCGC
1591	CATAAATTGGTTCACACCGC
1592	GAAACTCCAATTCAGCGGAC
1593	GAACAATGAATTTAGCGGCC
1594	TTCCATTAGATGTGATGCCC
1595	TATCATATCATCTGAGGCCC
1596	ATCAGAAGAACTGCACGTCC
1597	AGCACAAGAACTACGCGCTG
1598	AGCAAAGAACCATGCCGCGT
1599	TAAAGAGCAATGTGGCGTAC
1600	ITCAGGGCATTGAGCGTAAA
1601	TTAATGGGCTTGAGCGTATC
1602	TTAATGCGGTTGAGATCGAC
1603	GCAGGGATAGCAGATACATC
1604	TCAGGAGAGGCATCGCATCA
1605	TTATCTTAGGGATGCGGATC
1606	TGTGCTCTAGGTCATCCGAG
1607	TTGTATCTAGTGCGAGGCAA
1608	TATTATCTAGTATGCGCGGC
1609	TAGTTATCAGAGTGA CTGCG
1610	GTTAGATCATAGTCACCGCG
1611	GTTAGTATAGATTGGCCGAC
1612	GTGTTTATACGTTGAGCACG
1613	TTATCTGTAGTCATCGAGGC
1614	TGATACTGAGTTAGCGAGCT
1615	GTGATCTCAGAGCGCAGCTT
1616	CAGATGTCAAGACGCGGACT
1617	CTGGTCAGACAGCGGAATCT
1618	CGTGGCAGACAGCTAGATAT
1619	GTGCCGAGACTCCACTGTTA
1620	GCGGACAGCTCTCCTAGTAT
1621	ATGCACA ACTATCAAGCCTG
1622	GTGCTTTACTAGCGGAGCCA
1623	TAAATATCGTATAGGCGGCG
1624	TAATTCTACTATACGCGGGC
1625	TAAATCGTATGTAGCAGCGC
1626	TCCTTCACTGTAGGCTAGGC
1627	TCAGTTATATGAGCCGACTC
1628	TCACGTATATTGACTCCGAC
1629	TCACCGTATTCGAGGCGACA
1630	TCGTA CTGATTGACGGTGAT
1631	TCACAGCGGTGAGGTTACT
1632	ITCACGCGGTGCGAGTATCT
1633	TACTTGACGTGACTGCATCG
1634	CGTCACAGAGGACAGCATAC
1635	TCACTAGAGCGTCGAGCTGT
1636	TCTACAGTGTGTCAGAGTGA

Seq. Id	3' to 5' sequence
1637	CTACCTAATCGACAGCAGAG
1638	CACCGATAACTACAGCAGGG
1639	CAACGTCTAGGACAAGGCAG
1640	CACTAGCTCAGACAGACGAG
1641	GACTTTACAGTACGATCAGC
1642	GAACTGACTGACATCGAGA
1643	GAGACAGTCGAGCGATCAAT
1644	GCACTTGTACGTCCAGTCAG
1645	GTACACGGACTGCCAGCATA
1646	GTAATACGCTATCAGCAGAC
1647	CTAGATAGACATCACTCACG
1648	TAGACTCTCGATCAGCCGTA
1649	GACTTGACGTACAGCCGAA
1650	CTTATGCGACACTAGCTCGA
1651	CTGATGCTACACTAGGCACA
1652	GCAGACGCACTATCATATAC
1653	GCAGTAGACACTTCTCACGA
1654	GCAGGTACACTGACCGACTA
1655	GCACATCACTGCACGATAGA
1656	GCAATGACTTCGACTCCAGA
1657	GACAAGTCATTTACAGGCGA
1658	GTAAC TTGTTTGACAGTGCG
1659	GAACTGCATGGACAGCGTA
1660	GCAAGGACTGAGACATGCTT
1661	TGCGAGGTAGGTTATATCTC
1662	TGCGGAGAGTGATATACTTC
1663	GGCGTGAGAGCATTATATCT
1664	GTGCTGCGAGAGTATTATCT
1665	CCGCGTGTACCATATAATAC
1666	GAGCGTGGACGATATACACT
1667	GGCCGTGTACGATTATGACT
1668	GTAGCTTGACGATGCTGACT
1669	GTGCTGGTACTAGCTGCTCT
1670	TAATGTGACGTAGCCGACTC
1671	TACCGAGTGCGAGATGCTCA
1672	TACCGATGTCGATAGATCCA
1673	TCTCGTATAGGATGAGCAAC
1674	TCGTGAGTAGGATGCTTTCA
1675	TACGTGAGATGATGATCGCT
1676	TAGTCGGTAGCATGAGTCTA
1677	TAGTTCGAGGAGTAGTCATC
1678	TAGGTACAGTGCTGGATACT
1679	CTGCGTCAAGTGTGTAGAAT
1680	TGTGCGCTAGAGTCTGTCCT
1681	GGTGCGTCACGATCTCCTAT
1682	GTGTGGGTACTATGCCATCA
1683	GCTGATGTACTATCCATACC
1684	GCTAGATGACGATCAGGTAC



1733 CAGCTCTAAGCAGCACAGGA  
 1734 CAGGTCAAGCACATACCAGT  
 1735 CTGTGCAATCACGCCAGAGA  
 1736 CGGCGCAATAATGTCACAGA  
 1737 CGGGACATAATTGACACAGT  
 1738 AGGGCCAGACAATACACCGT  
 1739 GAGGTCACAATTTGCTACAC  
 1740 CAGGCACAAGATTGAGCACG  
 1741 ACAAGCGCAAATACTGCCGG  
 1742 ACAATCTGAAATAGCGCGGC  
 1743 ATCGACCCAAGAATAGCTCG  
 1744 ATAAGCACAAGCAGCGCGGT  
 1745 AACACTCCAAACCGAGGGTG  
 1746 AATCTATCAAAGCGACGGCC  
 1747 ATTCCCATAACGCGGAGGAC  
 1748 ATGCCAGCAACGCGCTAGAA  
 1749 ATGCTCACAAGCCACGAGAG  
 1750 ATGCTCCAACGATACATACG  
 1751 CAGCTTCAAGAGTACATACG  
 1752 CATGTCACAAGGGCATAGAC  
 1753 CATGGTCTAAGCCCTACAGA  
 1754 ACATGGCGAAAGCACCACGT  
 1755 CTTAGTTCAATGCACGCACG  
 1756 CGCCAGTTAATGCACGACAG  
 1757 CAGCAGCAACTCGACTAGAG  
 1758 CCGAAGTCAACTGCGCTAGA  
 1759 CCAAGTGCAATAAGAGACGT  
 1760 CCAGGCGAACTGATCGTAAA  
 1761 CCTGGTACAATCAGTAGCAA  
 1762 CTAGTGGCAATCATCAGACA  
 1763 CAATGCGAACTCACTAGACG  
 1764 CATGGCGTACCAATACCTAG  
 1765 AAGTGGCCCAAATAACTGCC  
 1766 CAAGGCCCAATACACAGGGT  
 1767 GATCTGCCAATGCCGCGATA  
 1768 GATTCGCCAATGTGCGCTAA  
 1769 GAGCCGCCAATGTCACTAGA  
 1770 GCGCCCGGAATGTCTATAT  
 1771 GCCGCGCCAATGTTACGTTA  
 1772 CTTGCGCCAATGCGTAGGAA  
 1773 TTCCCATGATCGCTGACGAG  
 1774 TTGCGGGAGCTGCCTCTTAA  
 1775 TTTCCCGGATAGCCGCTGTA  
 1776 TTTGCTGGAGTATGCGCTCA  
 1777 TTGTTCTCAGCTTGCGGCAG  
 1778 TGTGTGGCAGCTTAGTTCAC  
 1779 TCTTGGGTAGCATCTGTCAC  
 1780 TGGGTGTCAGCATCTACGCA

Seq. Id	3' to 5' sequence
1733	CAGCTCTAAGCAGCACAGGA
1734	CAGGTCAAGCACATACCAGT
1735	CTGTGCAATCACGCCAGAGA
1736	CGGCGCAATAATGTCACAGA
1737	CGGGACATAATTGACACAGT
1738	AGGGCCAGACAATACACCGT
1739	GAGGTCACAATTTGCTACAC
1740	CAGGCACAAGATTGAGCACG
1741	ACAAGCGCAAATACTGCCGG
1742	ACAATCTGAAATAGCGCGGC
1743	ATCGACCCAAGAATAGCTCG
1744	ATAAGCACAAGCAGCGCGGT
1745	AACACTCCAAACCGAGGGTG
1746	AATCTATCAAAGCGACGGCC
1747	ATTCCCATAACGCGGAGGAC
1748	ATGCCAGCAACGCGCTAGAA
1749	ATGCTCACAAGCCACGAGAG
1750	ATGCTCCAACGATACATACG
1751	CAGCTTCAAGAGTACATACG
1752	CATGTCACAAGGGCATAGAC
1753	CATGGTCTAAGCCCTACAGA
1754	ACATGGCGAAAGCACCACGT
1755	CTTAGTTCAATGCACGCACG
1756	CGCCAGTTAATGCACGACAG
1757	CAGCAGCAACTCGACTAGAG
1758	CCGAAGTCAACTGCGCTAGA
1759	CCAAGTGCAATAAGAGACGT
1760	CCAGGCGAACTGATCGTAAA
1761	CCTGGTACAATCAGTAGCAA
1762	CTAGTGGCAATCATCAGACA
1763	CAATGCGAACTCACTAGACG
1764	CATGGCGTACCAATACCTAG
1765	AAGTGGCCCAAATAACTGCC
1766	CAAGGCCCAATACACAGGGT
1767	GATCTGCCAATGCCGCGATA
1768	GATTCGCCAATGTGCGCTAA
1769	GAGCCGCCAATGTCACTAGA
1770	GCGCCCGGAATGTCTATAT
1771	GCCGCGCCAATGTTACGTTA
1772	CTTCGCGCAATGCGTAGGAA
1773	TTCCCATGATCGCTGACGAG
1774	TTGCGGGAGCTGCCTCTTAA
1775	TTTCCCGGATAGCCGCTGTA
1776	TTTGCTGGAGTATGCGCTCA
1777	TTGTTCTCAGCTTGCGGCAG
1778	TGTGTGGCAGCTTAGTTCAC
1779	TCTTGGGTAGCATCTGTCAC
1780	TGGGTGTCAGCATCTACGCA





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Seq. Id	3' to 5' sequence
1829	CTCGCTTACGACAGACTGGA
1830	CGCGCACGAGACATAGCTTA
1831	AGCGTCACACACAAGACTGG
1832	CCTACGAGACACATGACAGG
1833	CGCCGAGTACACATGCAGAT
1834	CCGTCGATACAGACTCAGAT
1835	CTCGTCAGACAGAGCGGATT
1836	GTCTCGCCACGTATCGGATT
1837	TCTCGCGTACTTAGGCATCA
1838	GTCTCGGTACGATGTAGCAA
1839	CGTGTGAGACAGTAGCATAT
1840	CGTGTAGCACAGCGACGATT
1841	GTGTAGCTCAGTCAGCATCA
1842	AGGTAGATAACGCTAGATCC
1843	CTGTAGAGACATCTGAATCC
1844	CTGATACGAAGTCTTATGCC
1845	CACGCTCGAAGACTAATGAC
1846	CACGCGATAAGACGTATAGC
1847	CTAGCAGTAAGTCTATGCAC
1848	CGTAGTTGAAGTCATCGACA
1849	CGCGATAGAAGTCAGGACAT
1850	GACGGACGACATCTGAGCAT
1851	CATAGACGAATACAGCGGGC
1852	GATCACGACCTACTAGCAGG
1853	AGATATAACGAACCTCTCGCG
1854	GATTATAGACTACTGAGGCC
1855	GAGTTTATACTACAGTGCCG
1856	GTCAC TTACGCTCAGGCAGA
1857	TCGCTAGACGCTCTGGCATA
1858	GTACGCTCAGCACTGGCATT
1859	GACGCGCTAATACTGTCACA
1860	GCGTGCATACGACTGCCATA
1861	TGTAGTCTAGTGCATGGTCA
1862	GTATAGTCAGAGCTGGCACC
1863	CGTCAGTCAAGTATGGCACA
1864	ACGAGAGTAAATATGCTGCC
1865	ATAGAGCGAACGATAGTTGC
1866	ATCTGACTAACGATGATGCC
1867	GTTGTAGGACGTATGATCTC
1868	TTAGTCGAGTCTATGAGCCC
1869	CGACGATACAGTAATCTAGC
1870	CTGATACAGGCATAGACATC
1871	GGTATCAGAGCTAGGACTAT
1872	TCTATCTCAGCTACGGTCGA
1873	TCAGTTCGATCTACGGCTAG
1874	TCAGTGCGACTCAGGTACGA
1875	GTCAGTGCCTCAGGCTAGA
1876	TAACGAGTCTTCAGCACGTA

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Seq. Id	3' to 5' sequence
1877	GAAGTCGCCTACATAGCCTA
1878	GAAGTCCGTTACATGACCAT
1879	GTCAGAGGATCGAGCCACTT
1880	GCGAGACAGGTCAGTACAAT
1881	CGTCAGAAGGCTCGCACATA
1882	GCATACAGGTTACGACGCCT
1883	GCGATACAGGTTACAGAGATA
1884	GGACGCATAGCTCGCAGTAT
1885	GGACGCAGATCGCAGCATAT
1886	CGGCGTTAATCGCAGAGAAC
1887	CGCGTTCTAAGGCACGGATA
1888	CGCGTCGCAAGGCTGTTATA
1889	CGATACGCAAGGCTACGACA
1890	CATCTAAGGACACTACACTG
1891	TATCATCGAGGACTCAGTGC
1892	CACCGAGCAAGACTGACATG
1893	CGCACCCGAAGTCAGAGATA
1894	CGGCTAGGAAGTCAGCATAA
1895	ATGCTGCGAACGCGCCATAA
1896	CCGCGTGCAACGTGTTTCATA
1897	GTCGCTGCATAGCATCTCAG
1898	GTCTGTGCATAGAGCGTCAT
1899	GTGGTGTCCTGATACGTCA
1900	GGTTAGCACTAGATCGCACT
1901	CGGGATCTACAGCATCATAG
1902	CTGGATATACAGCACTCACA
1903	ATGCGGCTAACGCCTCATAA
1904	TCGCGGCGCACTCTGTTATA
1905	TCGTGCTACTGCCACTGTAT
1906	TAGGACACTTCGCCACTATG
1907	TATGACAGTTCGCGCTACCG
1908	TCGCGCAGTTAGCCCTATGT
1909	TAGCCACCGTAGCTGATCGT
1910	GTAACCCGCTATCAGATCGA
1911	AGAGCGCAACACCACATTGT
1912	AGGCTAAGAACGCACACTCG
1913	GAGCCTAGACAGCTTCATAC
1914	GGCAGTTCACGACTCGACAT
1915	GGCCTTAGACGACTCGCATA
1916	GGTCGATCAGCACTGCATAC
1917	GGAGAGTCAGCACAGTCCTA
1918	GTATAGGCAGCACGGCTCAT
1919	GCACGGCGAGCACTATCTTA
1920	TAACGTCCTGCACGATCTGT
1921	GGACGCCTAGCACATCTGAT
1922	CGCTGCACATCACATGGATT
1923	GCACATCGAGCACATGCAGT
1924	GCACGACCAGCTCTTAGGAT

Seq. Id	3' to 5' sequence
1925	CCCACCAGACAGATAGAGGT
1926	CCCGACGCACGAATAGATAG
1927	CCCACGACAGATACATGAGT
1928	CTTCGCGCAGCTACATAGAT
1929	CGCTCCGAAGCTGCGATAAT
1930	CGCCGCGTAAGCAACAAATT
1931	CGACGCTCAAGGACTCATAA
1932	CGCACACTAAGGATCATTAC
1933	AGACACGCAAGAAGCTGGCT
1934	GCACGCATAGCAGAGGATCT
1935	GCTACGTCACCTGAGCAGGAT
1936	GTACATCTCGTGAGCAGAGC
1937	CTACACGACTTGAGACGAAG
1938	CTAAGTACGTGCAAGCAAGG
1939	GACACGTAGGACAGCTATGC
1940	GACATAGTAGACATCTCACG
1941	GACAGCGTAGACATCGTCAG
1942	GACTATCACGACATTCAGCG
1943	GATCTACACGCTACCAGTGG
1944	GCTTACTACGGATAGATCAG
1945	GCGTATCTAATGGAGTAGCA
1946	GCGTATTTACAGTGAGCGAC
1947	GCGTATATCGAATTGAGTGC
1948	GCGTTCACAGAGTCCACGAT
1949	CGCGTATCAAGGTCACGACA
1950	GCTATTACAGTGTCAGAGAC
1951	CGTCAGATAAGGTGAGTTAC
1952	CGTCTGTGAAGGTCAGCTAA
1953	TATTAGCACTCGTCAGCAGC
1954	ATGTTATCAACGTCAGCGAC
1955	GGCATACTAGAGTCAGCGAT
1956	AGTGCGATACAATACGAGCG
1957	CAGCACACAGAGTACAGCGT
1958	CGTAGCATAAGGTCAGCACC
1959	GTCCATAGACGTTGATACCA
1960	GCTACGATAGATGAGCCACG
1961	CGGAGTACACCAGATCCAGA
1962	GAGCGTATAGGAGATCCAAC
1963	GACTGTAGAGAGACGATCCA
1964	CTAGTAGGAAGTGCGATCAA
1965	CGTAGAGGAAGTGATACTCA
1966	CGTATCGGAAGTGAGTATCA
1967	CTATGACGAAGTGAGAGTAC
1968	GTTTCGTAGAGATGATCGTCA
1969	GTTCTCAGATAGTATGCAGC
1970	AGTCTGTAAAGATATGCGCC
1971	AGCACGGAACAGTAAGCCCT
1972	ATCCAGAGAACGTGAGATCC



Seq. Id	3' to 5' sequence
2022	GATCGTGAATCCGCGCACTA
2023	GAGCCGTAATCCGAGCGATA
2024	TACTCCTGACGACTTAGGCA
2025	TGCTGTCACTCGGCGTCTAT
2026	GTACTAGCATATCATCGACG
2027	TATCGCATAGATCAGTGAGC
2028	TACGGGCAGCCAGGTACTTT
2029	GTTTCATCACGAGTGCGTAGA
2030	CATGTATCAAGATGGCTGAC
2031	GGTCGCGCATTCCAGCATA
2032	GCACATATCTAGCGACATCT
2033	ACGCGGCTAAAGGTAGATAC
2034	CACTGCCCACAAGATGTAGA
2035	GGATTTACATGGCCTAGCAA
2036	CATGACACAGAATCGACCGT
2037	AGAGGCATAAATGAGTCTCC
2038	TGAGTAGTACGTTACGCCTG
2039	CGATAGCGAAGGAGTCCACA
2040	ACACTCTGAAAGACGCGACG
2041	GTCTTAATGTTGGGCAACG
2042	GTTATCGACTACGCTGTACT
2043	TCGTGAGACCGTCGTCAGTA
2044	GACAGCGCAGTACAGGTAAT
2045	CGTACAGTAAGTATGATGCC
2046	TAGAGCATCTGACGCTATGA
2047	GTCACGATTAGTAGGCACG
2048	TCGTACCTGTATTACGCGCG
2049	TTAATCCGCTGTAGCCCAA
2050	TTAATTGACTTCGCTCCAGC

## EXPERIMENTS

Arrays containing probes corresponding to SEQ ID NOS 1-2050 were designed and manufactured using known photolithography techniques. Four probes were designed to interrogate each sequence from SEQ ID NOS 1-2050: a probe designed to be the perfect match complement to the sequence (PM), a probe designed to have a central mismatch at position 10 (MM), and probes designed to be the complements to the PM and MM probes (cPM and cMM respectively).

FIG. 2 shows an example of the sequences attached to each of the four array features representing a given tag sequence. The first block contains the cPM probe. The second block contains the cMM probe. The third block contains the PM probe - the probe to which the tag is expected to hybridize with the highest affinity. The fourth block contains the MM probe.

FIG. 3 shows the array features from the above-described array. The array was hybridized with biotin-labeled oligonucleotide tags, stained with streptavidin-phycoerythrin, and the data was collected with a laser scanner. Four features, organized vertically on the probe array, represent each tag-probe. For each of the four tag-probes shown, arranged horizontally across the array, the brightest hybridization signal is seen with the “PM” feature.

FIG. 4 is a scanned image of the hybridization pattern resulting from the hybridization of 2050 different oligonucleotide tags labeled with phycoerythrin to an array designed as described above.

FIG. 5 is a scanned image of the hybridization pattern resulting from the hybridization of 50 sequences complementary to SEQ ID Nos. 2001-2050 to an array designed as described above.

FIG. 6 shows signal intensities from two different independent experiments in which 2000 biotinylated oligonucleotide tags or 50 fluorescein labeled control oligonucleotides were hybridized to arrays designed as described above. The frequency of results are shown as normalized (to scale of 0-1, in bins of 0.05) natural logarithms of the net signal intensities. The normalized natural logarithm of the signal intensities obtained are distributed about a geometric mean of 0.8 with a standard deviation of less than 0.1.

FIG. 7 shows the PM/MM ratios from the data described in FIG. 4 above. More than 98% of the hybridization's yielded a PM/MM ratio greater than 3/1.

## CONCLUSION

The above descriptions are illustrative and not restrictive. Many variations of the invention will become apparent to those of skill in the art upon review of this disclosure. The scope of the invention should, therefore, be determined not with reference to the above description, but instead should be determined with reference to the appended claims along with their full scope of equivalents.

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